#4

SEQUENCE LISTING

<110>   TransMIT Gesellschaft für Technologietransfer mbH
        TransMIT Gesellschaft für Technologietransfer mbH

<120>   Method for screening the allelic state at the 5'-flanking region of the
aS1 casein gene

<130>   An127/Pri

<140>   PCT/DE 03/02747
<141>   2003-08-15

<150>   DE 102 38 433 A1
<151>   2002-08-16

<160>   8

<170>   PatentIn version 3.1

<210>   1
<211>   18
<212>   DNA
<213>   Bos spec.

<220>
<221>   Primer 2
<222>   (1)..(18)
<223>   18 basepair, single stranded nucleic acid (linear)

<400>   1
gaagaagcag caagctgg   18

<210>   2
<211>   19
<212>   DNA
<213>   Bos spec.

<220>
<221>   Primer 3
<222>   (1)..(19)
<223>   19 basepair, single stranded nucleic acid (linear)

<400>   2
ccttgaaata ttctaccag   19

<210>   3
<211>   1061
<212>   DNA
<213>   Bos taurus

<220>
<221>   alpha-S1Kaseingen

<400>   3
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa   120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg   180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt   240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat   300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa   360

taaccataaa tctagggttt tgttggggtt ttttttttgtt tgttaatttta gaacaatgcc   420

attccatttc ctgtataatg agtcacttct ttgttgtaaa ctctccttag aatttcttgg   480

gagaggaact gaacagaaca ttgatttcct atgtgagaga attcttagaa tttaaataaa   540

cctgttggtt aaactgaaac cacaaaatta gcattttact aatcagtagg tttaaatagc   600

ttggaagcaa aagtctgcca tcaccttgat catcaaccca gcttgctgct tcttcccagt   660

cttgggttca aggtattatg tatacatata acaaaatttc tatgattttc ctctgtctca   720

tctttcattc ttcactaata cgcagttgta acttttctat gtgattgcaa gtattggtac   780

tttcctatga tatactgtta gcttaaaaat atatttgcaa atgttgatac tatctatctc   840

agagctatag gtgaaaaatt aaatactttt ataaagacca aattgatcat ttttaaacga   900

aattcttata tactgaaaat gtagatacat aacttcagta tagatttatg gtaaaataat   960

ttgaatcatt tttgtcaaat tctgtaaaaa gttgtcatac agaataattt ataatatttt   1020

tgttttcata gaaataacat ttctggtaga atatttcaag g   1061

<210> 4
<211> 652
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region from position 616 and Exon 1 at position 617
<222> (1)..(652)
<223> Mutation/SNP position 83 (A to G), position 98 (A to G), position 298 (A to C), position 442 (A to G; change/loss of YY1- and AP1 -bindingsite), position 541 (G to A);
deletion TT between position 389 and 394 compaired with Allel2

<400> 4
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aagtttatac aataattgta ttttcttttt gcaggaaaaa   120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg   180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt   240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcct ttacaggtat   300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa   360

taaccataaa tctagggttt tgttggggtt ttttgtttgt taatttagaa caatgccatt   420

ccatttcctg tataatgagt cgcttctttg ttgtaaactc tccttagaat ttcttgggag   480

aggaactgaa cagaacattg atttcctatg tgagagaatt cttagaattt aaataaacct   540

attggttaaa ctgaaaccac aaaattagca ttttactaat cagtaggttt aaatagcttg   600

gaagcaaaag tctgccatca ccttgatcat caacccagct tgctgctttc tt   652

<210> 5
<211> 654
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region and Exon 1
<222> (1)..(654)
<223> Bindingsite for transcriptionfactor AP-1 at position 438 to 445
Bindingsite for transcriptionfactor YY-1 at position 443 to 448

<400> 5
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa   120

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gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg      180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt      240

aataaaaatt gaaaaatttt gaagaccccca ttttgtccca agaatttcat ttacaggtat      300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360

taaccataaa tctagggttt tgttggggtt ttttttgttt gttaatttag aacaatgcca      420

ttccatttcc tgtataatga gtcacttctt tgttgtaaac tctccttaga atttcttggg      480

agaggaactg aacagaacat tgatttccta tgtgagagaa ttcttagaat ttaaataaac      540

ctgttggtta aactgaaacc acaaaattag cattttacta atcagtaggt ttaaatagct      600

tggaagcaaa agtctgccat caccttgatc atcaacccag cttgctgctt tctt           654
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<210> 6
<211> 650
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region
<222> (1)..(650)
<223> Bindingsite for transcriptionfactor AP-1 at position 434 to 441
      Bindingsite for transcriptionfactor YY-1 at position 439 to 444
      deletion G and TTT between 390 and 396 compaired with Allel 2

<400> 6
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gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg       60

gtataattaa aatgccacca aaatttatac aataattata ttttcttttt gcaggaaaaa      120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg      180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt      240

aataaaaatt gaaaaatttt gaagaccccca ttttgtccca agaatttcat ttacaggtat      300

tgaatttttc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa      360

taaccataaa tctagggttt tgttggggtt ttttttgtta atttagaaca atgccattcc      420

atttcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagag      480

gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt      540

tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga      600

agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt                650
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<210> 7
<211> 650
<212> DNA
<213> Bos taurus

<220>
<221> CSN1S1-gene, 5`flanking region
<222> (1)..(650)
<223> Bindingsite for transcriptionfactors: AP-1 at position 434 to 441
    , ABF1 at position 469 to 483, YY-1 at position 439 to 444;
    mutation (SNP) at position 480 (G to C), developing a ABF1-bindin
    gsite;
    deletion G and TTT between position 390 and 396 compaired with Al
    lel 2

<400> 7
gaatgaatga actagttacc acaactagta cacccaaaat gaacaaaaaa tagcttggtg   60

gtataattaa aatgccacca aaatttatac aataattata ttttctttтt gcaggaaaaa   120

gattagacca catataatgt aacttatttc acaaggtaaa taattataat aaataatatg   180

gattaactga gttttaaaag gtgaaataaa taatgaattc ttctcatggt cttgtatgtt   240

aataaaaatt gaaaaatttt gaagacccca ttttgtccca agaatttcat ttacaggtat   300

tgaattttтc aaaggttaca aaggaaattt tattgatata ataaatgcat gttctcataa   360

taaccataaa tctagggttt tgttggggtt ttttttgtta atttagaaca atgccattcc   420

atttcctgta taatgagtca cttctttgtt gtaaactctc cttagaattt cttgggagac   480

gaactgaaca gaacattgat ttcctatgtg agagaattct tagaatttaa ataaacctgt   540

tggttaaact gaaaccacaa aattagcatt ttactaatca gtaggtttaa atagcttgga   600

agcaaaagtc tgccatcacc ttgatcatca acccagcttg ctgctttctt   650

<210> 8
<211> 20
<212> DNA
<213> Bos spec.

<220>
<221> Primer1
<222> (1)..(20)
<223> 20 basepair, single stranded nucleic acid (linear)

<400> 8
gaatgaatga actagttacc   20